NEW SET OF CLAIMS

Claim 1) The use of a peptide with 10-25 amino-acid residues comprising:

i) two positively charged domains at neutral pH consisting of 3-9 amino-acid residues, of which two-thirds are cationic amino acids;

ii) between the said positively charged domains, a group of two or three non-cationic, amino-acid residues;

iii) at either N- or C-terminal extremity of the peptide, a group of 0 to 10, preferably 0 to 5, amino-acid residues chosen from the group comprising non-hydrophobic amino acids and positively charged amino acids, however, in the case of a positively charged amino-acid residue, the latter is not immediately adjacent to the positively charged domains,

for the preparation of pharmaceutical composition aimed at treating an infection by Gram-negative bacteria, in which composition the said peptide passes through the bacterial membrane in order to deliver to the interior of the bacteria an antibacterial compound to which it is associated in the said composition.

Claim 2) The use according to Claim 1, characterized in that in the said peptide (i), the positively charged cationic amino acids of the two domains are chosen from the group comprising arginine and lysine, and (ii) the non-cationic amino acids of the group between the said positively charged domains are non-hydrophobic amino acids, chosen, for example, from the group comprising glutamic acid, serine, glycine, leucine, and glutamine.

Claim 3) The use according to one of the Claims 1 or 2, characterized in that the peptide is chosen from the group comprising the following sequences: SEQ ID N0.1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, and SEQ ID NO:11.

Claim 4) The use according to any of the Claims 1 to 3, characterized in that the peptide is chosen from the group

comprising the following sequences: SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, and SEQ ID NO:7.

Claim 5) The use according to any of the Claims 1 to 4, characterized in that the anti-bacterial compound is chosen from those presenting physiochemical properties rendering them incapable of passing through the membrane of the Gram-negative bacteria.

Claim 6) The use according to any of the preceding claims, characterized in that the anti-bacterial compound is hydrophobic.

Claim 7) The use according to any of the preceding claims, characterized in that the anti-bacterial compound is chosen from the group comprising the following compounds: antibiotics of the family of macrolides, ketolides, such as erythromycin, clarithromycin, azithromycin, and telithromycin.

Claim 8) The use according to any of the preceding, characterized in that the antibacterial pharmaceutical composition comprises the association of at least one peptide as defined in the said claims and at least one antibacterial compound either in the form of a mixture or as a product in which one or more identical or different peptides are covalently bound to one or more identical or different antibacterial compounds, possibly by means of a spacer arm.

Claim 9) The use according to Claim 8, characterized in that the antibacterial pharmaceutical composition comprises a product with the following formula (I):

$$(A\text{-})_m(X)_p(\text{-}P)_n \quad (I)$$

where A is the residue of an anti-bacterial compound, P is the residue of a peptide, as defined in the preceding claims, and X represents either a covalent bond between A

and P or a spacer arm linking at least an A residue to at least a P residue, m is an integer from 1 to 3, n is an integer from 1 to 3, and p represents zero or an integer at the most equal to the greater of the numbers m and n.

Claim 10) An antibacterial composition characterized in that it comprises the association of at least one peptide and at least an antibacterial compound, either in the form of a mixture or a product in which one or more identical or different peptides are covalently bound to one or more identical or different antibacterial compounds, possibly by means of a spacer arm, and the said peptide is chosen from the group comprising the following sequences: SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, and SEQ ID NO:11.

Claim 11) An antibacterial composition characterized in that it comprises an association of at least one peptide and one antibacterial compound either in the form of a mixture or a product in which one or ore identical or different peptides are covalently bound to one or more identical or different antibacterial compounds, possibly by means of a spacer arm, and in that the said peptide is chosen from the group comprising the following sequences: SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, and SEQ ID NO:7.

Claim 12) A product of the following formula (I):

$(A\text{-})_m(X)_p(\text{-}P)_n$ (I)

where A, X, m, p and n are defined as in Claim 9, and P is the residue of a peptide chosen from the group comprising the following sequences: SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ 25 ID NO. 4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, and SEQ ID NO:11.

Claim 13) A product of with the following formula (I):

$(A\text{-})_m(X)_p(\text{-}P)_n$ (I)

where A, X, m, p and n are defined as in Claim 9, and P is the residue of a peptide chosen from the group comprising

the following sequences: SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, and SEQ ID NO:7.